



Findings from the surveillance of avian influenza in wild birds and poultry in Denmark

Hjulsager, Charlotte Kristiane

Publication date:
2016

Document Version
Peer reviewed version

[Link back to DTU Orbit](#)

Citation (APA):
Hjulsager, C. K. (2016). *Findings from the surveillance of avian influenza in wild birds and poultry in Denmark*. Abstract from Nordic Poultry Conference 2016, Billund, Denmark.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Abstract for Nordic Poultry Conference, Billund, Denmark, 7th-9th November 2016.

Findings from the surveillance of avian influenza in wild birds and poultry in Denmark

By Charlotte Kristiane Hjulsager, Virology group, Section for Diagnostics and Scientific Advice, Technical University of Denmark.

Avian influenza (AI) is a highly contagious disease that can affect all bird species. The clinical signs include respiratory disease, lethargy, drop in egg production, neurological signs, hemorrhages in shanks, swollen wattles, combs and eyes, and mortality. The severity of disease depends on the virus strain and species of bird, and varies from a subclinical to a highly pathogenic form with up to 100 % mortality within 48 hours. AI is of high economic importance for the poultry production worldwide. Elimination of the disease is a common goal, and in EU, the disease is mainly controlled by surveillance and stamping out procedures.

AI is caused by influenza virus type A, which is divided into subtypes based on the surface glycoproteins haemagglutinin (HA) and neuraminidase (NA). At present, 16 HA (H1-H16) and 9 NA (N1-N9) subtypes have been recognized in birds. Each virus has one HA and one NA subtype and is named accordingly, e.g. H1N2, H5N8, H7H1. AI viruses are also classified according to the degree of the disease that they cause in chickens. Low pathogenic AI (LPAI) viruses replicate in limited tissues and cause mild or no clinical disease, whereas highly pathogenic AI viruses (HPAI) can replicate in more tissues leading to a systemic infection often characterized by high mortality. Only viruses of subtypes H5 and H7 are known to cause HPAI, but these subtypes also exist as LPAI viruses. It appears that HPAI viruses arise by mutation of LPAI viruses. The factors that governs the transition have not been fully elucidated, but based on the experience from HPAI virus occurrence and outbreaks, it is anticipated that the wide circulation in a poultry flock that happens when a LPAI virus is introduced, will raise the chance that mutation to HPAI occurs.

Surveillance of AI has been conducted in Denmark since 2003. The surveillance is mainly targeted subtypes H5 and H7 because these can manifest as HPAI. The surveillance consists of

- Serological surveillance of poultry with virological follow-up in H5/H7 seropositive flocks
- Virological surveillance of game birds for restocking
- Passive surveillance in poultry
- Active and passive virological surveillance in wild birds

HPAI has only been detected at Danish territory in 2006. Outbreaks of H5/H7 LPAI are a rare event in Danish poultry. Since 2003 there have been 10 such outbreaks, whereas H5/H7 LPAI viruses have been detected every year in wild birds. The viruses have been characterized by sequencing, and comparisons by phylogenetic analyses suggest that AI virus genes and whole viruses are exchanged between poultry and wild birds and among wild birds. The detailed characterization of viruses by sequencing allows tracing of AI virus outbreaks to facilitate control of the disease.